

WO 00/39157

PCT/CA99/01224

1/5

## SEQUENCE LISTING

&lt;110&gt; Connaught Laboratories Limited

&lt;120&gt; Chlamydia antigens and corresponding DNA fragments and uses thereof

&lt;130&gt; 77813-6

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; US 60/114,060

&lt;151&gt; December 28, 1998

&lt;150&gt; US 60/123,967

&lt;151&gt; March 12, 1999

&lt;150&gt; US 60/141,271

&lt;151&gt; June 30, 1999

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1637

&lt;212&gt; DNA

&lt;213&gt; Chlamydia pneumoniae

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)..(1595)

&lt;400&gt; 1

```

gaaataaaaa actatcagaa tagaaaataa aagtatttca gagggtaa atg aca      56
                                   Met Thr
                                   1

aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg      104
Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro
              5                      10                      15

ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc      152
Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe
              20                      25                      30

ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act      200
Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr
              35                      40                      45                      50

ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc      248
Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile
              55                      60                      65

aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat      296
Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr
              70                      75                      80

gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg      344
Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val
              85                      90                      95

```

WO 00/39157

PCT/CA99/01224

2/5

gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat	392
Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr	
100 105 110	
ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag	440
Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln	
115 120 125 130	
gcc atc cta cct cca gga ttg cta gga ctc gtt gcc atc tta aga aac	488
Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn	
135 140 145	
tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc	536
Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val	
150 155 160	
atg cta tct cta atg ttc tgg gga ttt gct aat gaa att aca aaa atc	584
Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile	
165 170 175	
cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att	632
His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile	
180 185 190	
tct tta cta gct tct ggt cgt gca att gtt tgg gct tca aag ttg aga	680
Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys Leu Arg	
195 200 205 210	
gct tcc gtt tct gaa ggt gta gat cct tgg gga att tct tta cgt ctt	728
Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu Arg Leu	
215 220 225	
ttg atg gct atg act att gta tct gga ctt gtt ctt atg gcc agt tac	776
Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala Ser Tyr	
230 235 240	
tgg tgg atc aat aag aac gta ttg acc gat cct cgc ttc tat aat cca	824
Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr Asn Pro	
245 250 255	
gaa gaa atg caa aag ggg aaa aaa ggt gct aaa cct aaa atg aat atg	872
Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met Asn Met	
260 265 270	
aaa gat agc ttc ctc tat ctt gat aga tct cct tat att ctt tta tta	920
Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu Leu Leu	
275 280 285 290	
act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg	968
Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val	
295 300 305	
act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat	1016
Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr	
310 315 320	
agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta	1064
Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val	
325 330 335	

WO 00/39157

PCT/CA99/01224

3/5

```

ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg 1112
Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp
    340                      345                      350

tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc 1160
Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile
    355                      360                      365                      370

gtt ttc ttc gct ctt gtt atc ttt aga aac caa gct tct ggg ctg gtc 1208
Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val
                      375                      380                      385

gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct 1256
Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala
                      390                      395                      400

ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca 1304
Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser
                      405                      410                      415

act aaa gaa atg gcc tat atc cct ctt gac caa gag caa aaa gtc aaa 1352
Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys
                      420                      425                      430

ggt aag gct gct att gat gta gtt gcc gcc cgc ttc gga aaa tca gga 1400
Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly
    435                      440                      445                      450

gga gct tta atc caa caa ggt ttg ctc gtt atc tgt gga agt att gga 1448
Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly
                      455                      460                      465

gct atg acc cct tat ctt gca gtg att ctt ctt ttc atc att gct att 1496
Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile
                      470                      475                      480

tgg ttg gtt tct gca act aag tta aac aaa cta ttc tta gcg cag tct 1544
Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser
                      485                      490                      495

gct ctt aaa gaa caa gaa gtg gct caa gaa gat tca gct cct gct tct 1592
Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser
    500                      505                      510

tca tagagttgct tctcttactc ttgttgatcc ctacctgctt tt 1637
Ser
515

```

<210> 2  
 <211> 515  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 2  
 Met Thr Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu  
 1 5 10 15  
 Trp Pro Ile His Thr His Glu Leu Lys Val Leu Pro Met Phe Leu  
 20 25 30

WO 00/39157

PCT/CA99/01224

4/5

Met Phe Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys  
                   35                                  40                                  45

Asp Thr Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro  
           50                                  55                                  60

Phe Ile Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu  
   65                                  70                                  75                                  80

Ile Tyr Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr  
                                   85                                  90                                  95

Ala Val Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val  
                                   100                                  105                                  110

Ile Tyr Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg  
           115                                  120                                  125

Leu Gln Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu  
   130                                  135                                  140

Arg Asn Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly  
  145                                  150                                  155                                  160

Ser Val Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr  
                                   165                                  170                                  175

Lys Ile His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala  
                                   180                                  185                                  190

Asn Ile Ser Leu Leu Ala Ser Gly Arg Ala Ile Val Trp Ala Ser Lys  
           195                                  200                                  205

Leu Arg Ala Ser Val Ser Glu Gly Val Asp Pro Trp Gly Ile Ser Leu  
   210                                  215                                  220

Arg Leu Leu Met Ala Met Thr Ile Val Ser Gly Leu Val Leu Met Ala  
  225                                  230                                  235                                  240

Ser Tyr Trp Trp Ile Asn Lys Asn Val Leu Thr Asp Pro Arg Phe Tyr  
                                   245                                  250                                  255

Asn Pro Glu Glu Met Gln Lys Gly Lys Lys Gly Ala Lys Pro Lys Met  
                                   260                                  265                                  270

Asn Met Lys Asp Ser Phe Leu Tyr Leu Asp Arg Ser Pro Tyr Ile Leu  
           275                                  280                                  285

Leu Leu Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile  
   290                                  295                                  300

Glu Val Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn  
  305                                  310                                  315                                  320

Asp Tyr Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val  
                                   325                                  330                                  335

Ser Val Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe  
                                   340                                  345                                  350

SUBSTITUTE SHEET (RULE 26)

WO 00/39157

PCT/CA99/01224

5/5

Gly Trp Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr  
 355 360 365  
 Gly Ile Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly  
 370 375 380  
 Leu Val Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val  
 385 390 395 400  
 Gly Ala Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe  
 405 410 415  
 Asp Ser Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys  
 420 425 430  
 Val Lys Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys  
 435 440 445  
 Ser Gly Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser  
 450 455 460  
 Ile Gly Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile  
 465 470 475 480  
 Ala Ile Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala  
 485 490 495  
 Gln Ser Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro  
 500 505 510  
 Ala Ser Ser  
 515

<210> 3  
 <211> 43  
 <212> DNA  
 <213> Chlamydia pneumoniae

<220>  
 <400> 3

ataagaatgc ggccgccacc atgacaaaaa ccgaagaaaa acc

43

<210> 4  
 <211> 29  
 <212> DNA  
 <213> Chlamydia pneumoniae

&lt;220&gt;

&lt;400&gt; 4

gcgccgcatc cctgaagaag caggagctg

29